# SEQUENCE LISTING

(1) GENERAL	INFORMATION:
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- 5 (i) APPLICANT: Ashkenazi, Avi J.
  - (ii) TITLE OF INVENTION: Apo-2 LI AND Apo-3 POLYPEPTIDES
  - (iii) NUMBER OF SEQUENCES: 11

- (iv) CORRESPONDENCE ADDRESS:
  - (A) ADDRESSEE: Genentech, Inc.
  - (B) STREET: 460 Point San Bruno Blvd
  - (C) CITY: South San Francisco
  - (D) STATE: California
  - (E) COUNTRY: USA
  - (F) ZIP: 94080
  - (v) COMPUTER READABLE FORM:
    - (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
    - (B) COMPUTER: IBM PC compatible
    - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
    - (D) SOFTWARE: WinPatin (Genentech)
- (vi) CURRENT APPLICATION DATA:
  - (A) APPLICATION NUMBER:
  - (B) FILING DATE: 31-Mar-1997
  - (C) CLASSIFICATION:
- 30 (vii) PRIOR APPLICATION DATA:
  - (A) APPLICATION NUMBER: 08/625328
  - (B) FILING DATE: 1-Apr-1996
  - (vii) PRIOR APPLICATION DATA:
- 35 (A) APPLICATION NUMBER: 08/710802



# (B) FILING DATE: 23-Sep-1996

(viii) ATTORNEY/AGENT INFORM	<b>ITA</b>	ON:
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- (A) NAME: Marschang, Diane L.
- (B) REGISTRATION NUMBER: 35,600
- (C) REFERENCE/DOCKET NUMBER: P1007P1

### (ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: 415/225-5416
- (B) TELEFAX: 415/952-9881
- (C) TELEX: 910/371-7168

# (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 181 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu 15 1 5 10

Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr Arg Ser 25 30 20

Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu 35 40 45

Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro 60 50 55

Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln 70 65

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Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala 80 85 90

Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu 95 100 105

Asn Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro Gly
110 115 120

0 Trp Phe Val Glu Cys Gln Val Ser Gln Cys Val Ser Ser Pro 125 130 135

Phe Tyr Cys Gln Pro Cys Leu Asp Cys Gly Ala Leu His Arg His
140 145 150

Thr Arg Leu Cys Ser Arg Arg Asp Thr Asp Cys Gly Thr Cys
155 160 165

Leu Pro Gly Phe Tyr Glu His Gly Asp Gly Cys Val Ser Cys Pro 170 175 180

Thr 181

# (2) INFORMATION FOR SEQ ID NO:2:

# (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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TGCCGGTGAC TTCCACAAGA AGATTGGTCT GTTTTGTTGC AGAGGCTGCC 100

CAGCGGGGCA ACTACCTGAA GGCCCCTTGC ACGGAGCCCT GCGCAACTCC 150

ACCTGCCTTG TGTGTCCCCA AGACACCTTC TTGGCCTGGG AGAACCACCA 200

TAATTCTGAA TGTGCCCGCT GCCAGGCCTG TGATGAGCAG GCCTCCCAGG 250

TGGCGCTGGA GAACTGTTCA GCAGTGGCCG ACACCCGCTG TGGCTGTAAG 300

CAGGGCTGGT TTGTGGAGTG CCAGGGTCAG CCAATGTGTC AGCAGTTTCA 350

CCCTTCTAAT GCCAACCATG CCTAGACTGC GGGGCCCTGC AACGCAACAC 400

ACGGCTAATN TGTTTCCCGC AGAGATNATT GTT 433

- (2) INFORMATION FOR SEQ ID NO:3:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 28 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
- 30 CCCGCTGCCA GGCCTGTGAT GAGCAGGC 28
  - (2) INFORMATION FOR SEQ ID NO:4:
    - (i) SEQUENCE CHARACTERISTICS:
      - (A) LENGTH: 28 base pairs

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- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear
- 5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

### CAGGGCCCCG CAGTCTAGGC ATGGTTGG 28

- 10 (2) INFORMATION FOR SEQ ID NO:5:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1438 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GAATTCCGGC GCGGAGGCCG AGAGAGAGT CACTTGCCCT GGCTCTACCT 50
TGAAGTGGTT CTCAGGGTTG GGGCGAGAGT CGGGGTGGGG ACCGAGATGC 100
AGCTCTATCC TGTGCCCCTG GTCGCAGCAG GCAGCCCAGC GCTTCGCGTG 150
TTCTACTTGG CCTGTCCGCT GCCGCCTAAT GAGCTCAGGT CTAGGCCGAG 200
CAGAGGGGGC ACCTGGTCGG ACTCGGTTGG GCTCGGGCGG CCCCGCCTCC 250
CCCCGCCCGC CAGGCGGGCC CTTCTCGACG GCGCGGGGCG GGCCCTGCGG 300
GCGCGGGGCT GAAGGCGGAA CCACGACGGG CAGAGAGCAC GGAGCCGGGA 350
AGCCCCTGGG CGCCCGTCGG AGGGCTATGG AGCAGCGGCC GCGGGGCTGC 400

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GCGGCGGTGG CGGCGCGCT CCTCCTGGTG CTGCTGGGGG CCCGGGCCCA 450 GGGCGGCACT CGTAGCCCCA GGTGTGACTG TGCCGGTGAC TTCCACAAGA 500 AGATTGGTCT GTTTTGTTGC AGAGGCTGCC CAGCGGGGCA CTACCTGAAG 550 GCCCCTTGCA CGGAGCCCTG CGGCAACTCC ACCTGCCTTG TGTGTCCCCA 600 AGACACCTTC TTGGCCTGGG AGAACCACCA TAATTCTGAA TGTGCCCGCT 650 GCCAGGCCTG TGATGAGCAG GCCTCCCAGG TGGCGCTGGA GAACTGTTCA 700 GCAGTGGCCG ACACCCGCTG TGGCTGTAAG CCAGGCTGGT TTGTGGAGTG 750 CCAGGTCAGC CAATGTGTCA GCAGTTCACC CTTCTACTGC CAACCATGCC 800 TAGACTGCGG GGCCCTGCAC CGCCACACAC GGCTACTCTG TTCCCGCAGA 850 GATACTGACT GTGGGACCTG CCTGCCTGGC TTCTATGAAC ATGGCGATGG 900 CTGCGTGTCC TGCCCCACGT AATTCCTAGC TGTCGTGGGA TGGAGGGAAG 950 GGCGGCTGGG AGCAGAGCAG GGGCCTGGGG TGGGGCAGGT GCTGCTGGTT 1000 CAGGAATAGG AAGAGGGGAT AGGGAGGAGG GAGCCTTGGC CCTGTGATGG 1050 GTGGGCCCA CTTCAGGCAA ACTTAGATGG CAAAAGAGCA ATCTGGATCC 1100 GCCTTAGCCA GATACATAAG GGTATTTGCC TTCACTTTCA GCCAGCATTC 1150 CCCCAGCGA TCCTAGCCAG ATATTACAGA TGATTTGTCA CTTACACAGA 1200 GAGTCACATT GATATAGCTT TAAAACTTGG GCTGAAGGAG GTTGAGGCTG 1250 CAGTGAGCTA TGATCGTGCC ACTGCACTTC AGCCTGGGCA ACAGAGCGAG 1300

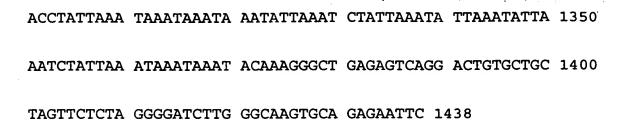
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## (2) INFORMATION FOR SEQ ID NO:6:

1:1	CECTEMOR	CHARACTERISTICS
<b>\ L /</b>	SECUENCE	CHARACIERISTICS

(A) LENGTH: 417 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Gln Arg Pro Arg Gly Cys Ala Ala Val Ala Ala Ala Leu 1 5 10 15

Leu Leu Val Leu Cly Ala Arg Ala Gln Gly Gly Thr Arg Ser
20 25 30

Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys Lys Ile Gly Leu 35 40 45

Phe Cys Cys Arg Gly Cys Pro Ala Gly His Tyr Leu Lys Ala Pro
50 55 60

Cys Thr Glu Pro Cys Gly Asn Ser Thr Cys Leu Val Cys Pro Gln
65 70 75

Asp Thr Phe Leu Ala Trp Glu Asn His His Asn Ser Glu Cys Ala 80 85 90

Arg Cys Gln Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu 95 100 105





	Asn	Сув	Ser	Ala	Val	Ala	Asp	Thr	Arg	Cys 115	Gly	Cys	Lys	Pro	Gly 120
5	Trp	Phe	Val	Glu	Cys 125	Gln	Val	Ser	Gln	Cys 130	Val	Ser	Ser	Ser	Pro 135
	Phe	Tyr	Cys	Gln	Pro 140	Cys	Leu	Asp	Cys	Gly 145	Ala	Leu	His	Arg	His 150
10	Thr	Arg	Leu	Leu	Cys 155	Ser	Arg	Arg	Asp	Thr 160	Asp	Cys	Gly	Thr	Cys 165
<b>\$</b> c	Leu	Pro	Gly	Phe	Tyr 170		His	Gly	Asp	Gly 175	Cys	Val	Ser	Cys	Pro 180
바이 의 그 근 크나 <mark>o</mark>	Thr	Ser	Thr	Leu	Gly 185	Ser	Cys	Pro	Glu	Arg 190	Cys	Ala	Ala	Val	Cys 195
	Gly	Trp	Arg	Gln	Met 200	Phe	Trp	Val	Gln	Val 205	Leu	Leu	Ala	Gly	Leu 210
H	Val	Val	Pro	Leu	Leu 215	Leu	Gly	Ala	Thr	Leu 220	Thr	Tyr	Thr	Tyr	Arg 225
<u>-</u> 25		Cys	Trp	Pro	His 230	Lys	Pro	Leu	Val	Thr 235	Ala	Asp	Glu	Ala	Gly 240
30	Met	Glu	Ala	Leu	Thr 245	Pro	Pro	Pro	Ala	Thr 250	His	Leu	Ser	Pro	Leu 255
	Asp	Ser	Ala	His	Thr 260	Leu	Leu	Ala	Pro	Pro 265	Asp	Ser	Ser	Glu	Lys 270
35	Ile	Cys	Thr	Val	Gln 275	Leu	Val	Gly	Asn	Ser 280	Trp	Thr	Pro	Gly	Tyr 285

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Pro	Glu		Gln	Glu 290	Ala	•			•				Se
Asp	Gln	Leu	Pro	Ser	Arg	Ala	Leu	Gly	Pro 310	Ala	Ala	Ala	Pr
Leu	Ser	Pro	Glu	Ser 320	Pro	Ala	Gly	Ser	Pro 325	Ala	Met	Met	Lei
Pro	Gly	Pro	Gln	Leu 335	Tyr	Asp	Val	Met	Asp 340	Ala	Val	Pro	Ala
Arg	Trp	Lys	Glu	Phe 350	Val	Arg	Thr	Leu	Gly 355	Leu	Arg	Glu	Ala
Ile	Glu	Ala	Val	Glu 365	Val	Glu	Ile	Gly	Arg 370	Phe	Arg	Asp	Glı
Tyr	Glu	Met	Leu	Lys 380	Arg	Trp	Arg	Gln	Gln 385	Gln	Pro	Ala	Gly
Gly	Ala	Val	Tyr	Ala 395	Ala	Leu	Glu	Arg	Met	Gly	Leu	Asp	Gl
Val	Glu	Asp	Leu	Arg	Ser	Arg	Leu	Gln	Arg 415	Gly	Pro 417		

# (2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

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# (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

### GGCGCTCTGG TGGCCCTTGC AGAAGCC 27

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- (2) INFORMATION FOR SEQ ID NO:8:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 25 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

TTCGGCCGAG AAGTTGAGAA ATGTC 25

- (2) INFORMATION FOR SEQ ID NO:9:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1634 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
- 30 CGGGCCCTGC GGGCGCGGGG CTGAAGGCGG AACCACGACG GGCAGAGAGC 50
  - ACGGAGCCGG GAAGCCCCTG GGCGCCCGTC GGAGGGCT ATG GAG 94
    Met Glu

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- 5 CTC CTG GTG CTG CTG GGG GCC CGG GCC CAG GGC GGC ACT 172
  Leu Leu Val Leu Leu Gly Ala Arg Ala Gln Gly Gly Thr
  20 25
- CGT AGC CCC AGG TGT GAC TGT GCC GGT GAC TTC CAC AAG 211

  10 Arg Ser Pro Arg Cys Asp Cys Ala Gly Asp Phe His Lys

  30 35 40
  - AAG ATT GGT CTG TTT TGT TGC AGA GGC TGC CCA GCG GGG 250 Lys Ile Gly Leu Phe Cys Cys Arg Gly Cys Pro Ala Gly 45 50
  - CAC TAC CTG AAG GCC CCT TGC ACG GAG CCC TGC GGC AAC 289
    His Tyr Leu Lys Ala Pro Cys Thr Glu Pro Cys Gly Asn
    55 60 65
  - TCC ACC TGC CTT GTG TGT CCC CAA GAC ACC TTC TTG GCC 328

    Ser Thr Cys Leu Val Cys Pro Gln Asp Thr Phe Leu Ala

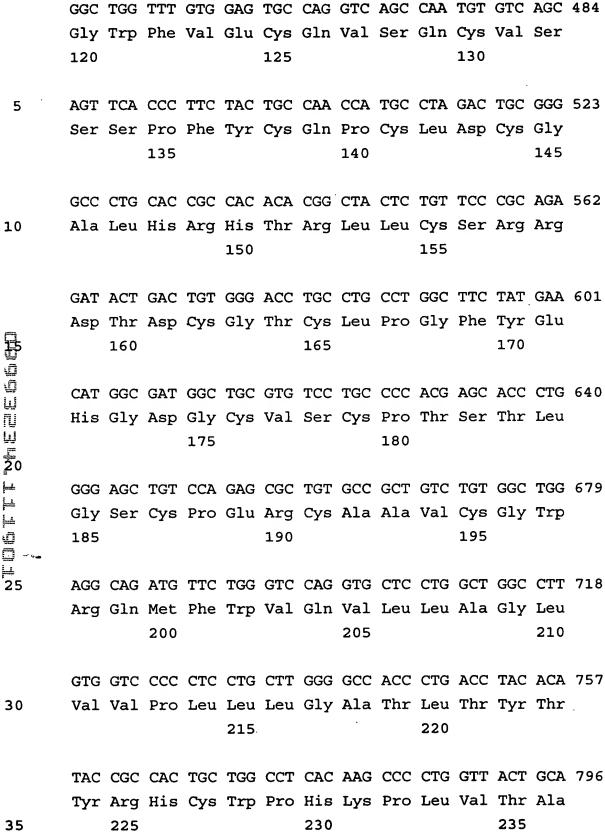
    70 75 80
  - TGG GAG AAC CAC CAT AAT TCT GAA TGT GCC CGC TGC CAG 367
    Trp Glu Asn His His Asn Ser Glu Cys Ala Arg Cys Gln
    85
    90
- GCC TGT GAT GAG CAG GCC TCC CAG GTG GCG CTG GAG AAC 406

  Ala Cys Asp Glu Gln Ala Ser Gln Val Ala Leu Glu Asn

  95

  100

  105
  - TGT TCA GCA GTG GCC GAC ACC CGC TGT GGC TGT AAG CCA 445 Cys Ser Ala Val Ala Asp Thr Arg Cys Gly Cys Lys Pro 110 115







GAT	GAA	GCT	GGG	ATG	GAG	GCT	CTG	ACC	CCA	CCA	CCG	GCC	835
Asp	Glu	Ala	Gly	Met	Glu	Ala	Leu	Thr	Pro	Pro	Pro	Ala	
			240					245					

- 5 ACC CAT CTG TCA CCC TTG GAC AGC GCC CAC ACC CTT CTA 874
  Thr His Leu Ser Pro Leu Asp Ser Ala His Thr Leu Leu
  250 255 260
- GCA CCT CCT GAC AGC AGT GAG AAG ATC TGC ACC GTC CAG 913

  10 Ala Pro Pro Asp Ser Ser Glu Lys Ile Cys Thr Val Gln

  265 270 275
  - TTG GTG GGT AAC AGC TGG ACC CCT GGC TAC CCC GAG ACC 952 Leu Val Gly Asn Ser Trp Thr Pro Gly Tyr Pro Glu Thr 280 285
  - CAG GAG GCG CTC TGC CCG CAG GTG ACA TGG TCC TGG GAC 991
    Gln Glu Ala Leu Cys Pro Gln Val Thr Trp Ser Trp Asp
    290 295 300
  - CAG TTG CCC AGC AGA GCT CTT GGC CCC GCT GCT GCG CCC 1030
    Gln Leu Pro Ser Arg Ala Leu Gly Pro Ala Ala Pro
    305
    310
  - ACA CTC TCG CCA GAG TCC CCA GCC GGC TCG CCA GCC ATG 1069
    Thr Leu Ser Pro Glu Ser Pro Ala Gly Ser Pro Ala Met
    315 320 325
- ATG CTG CAG CCG GGC CCG CAG CTC TAC GAC GTG ATG GAC 1108

  Met Leu Gln Pro Gly Pro Gln Leu Tyr Asp Val Met Asp

  330 335 340
  - GCG GTC CCA GCG CGG CGC TGG AAG GAG TTC GTG CGC ACG 1147
    Ala Val Pro Ala Arg Arg Trp Lys Glu Phe Val Arg Thr

    345
    350

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CTG GGG CTG CGC GAG GCA GAG ATC GAA GCC GTG GAG GTG 1186 Leu Gly Leu Arg Glu Ala Glu Ile Glu Ala Val Glu Val 355 360 365

GAG ATC GGC CGC TTC CGA GAC CAG CAG TAC GAG ATG CTC 1225
Glu Ile Gly Arg Phe Arg Asp Gln Gln Tyr Glu Met Leu
370
375

AAG CGC TGG CGC CAG CAG CCC GCG GGC CTC GGA GCC 1264

10 Lys Arg Trp Arg Gln Gln Pro Ala Gly Leu Gly Ala

380 385 390

GTT TAC GCG GCC CTG GAG CGC ATG GGG CTG GAC GGC TGC 1303

Val Tyr Ala Ala Leu Glu Arg Met Gly Leu Asp Gly Cys

395

400

405

GTG GAA GAC TTG CGC AGC CGC CTG CAG CGC GGC CCG T 1340

Val Glu Asp Leu Arg Ser Arg Leu Gln Arg Gly Pro

410

415

417

- (2) INFORMATION FOR SEQ ID NO:10:
  - (i) SEQUENCE CHARACTERISTICS:





- (A) LENGTH: 29 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Single
- (D) TOPOLOGY: Linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
- ATCAGGGACT TTCCGCTGGG GACTTTCCG 29

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- (2) INFORMATION FOR SEQ ID NO:11:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 30 base pairs
    - (B) TYPE: Nucleic Acid
    - (C) STRANDEDNESS: Single
    - (D) TOPOLOGY: Linear
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

AGGATGGGAA GTGTGTGATA TATCCTTGAT 30